

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Opperman, Hermann
Ozkaynak, Engin
Rueger, David C.
Kuberasampath, Thangavel
- (ii) TITLE OF INVENTION: Osteogenic Proteins
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Lahive & Cockfield
 - (B) STREET: 60 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch,
720kb storage
 - (B) COMPUTER: IBM XT
 - (C) OPERATING SYSTEM: DOS 3.30
 - (D) SOFTWARE: Word Perfect 5.0
- (vi) CURRENT APPLICATION DATA:
 - (B) FILING DATE: 18-Oct-90
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 569,920
 - (B) FILING DATE: 20-Aug-90
 - (C) APPLICATION NUMBER: US 315,342
 - (D) FILING DATE: 23-Feb-89
 - (E) APPLICATION NUMBER: US 422,699
 - (F) FILING DATE: 17-Oct-89

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
10					15			
Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45
Arg	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		

Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His.					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1930 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bovinae

(F) TISSUE TYPE: bone

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: mouse embryo

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGAATTCCGC	TGCCAGGCAC	AGGTGCGCCG	TCTGGTCCTC	40
CCCGTCTGGC	GTCAGCCGAG	CCCGACCAGC	TACCA GTGGA	80
TGCGCGCCGG	CTGAAAGTCC	GAG ATG GCT	ATG CGT	115
		Met Ala Met Arg		
		1		
CCC GGG CCA CTC	TGG CTA TTG	GGC CTT GCT	CTG	148
Pro Gly Pro Leu	Trp Leu Leu Gly	Leu Ala Leu		
5	10	15		
TGC GCG CTG GGA	GGC GGC CAC	GGT CCC GGT	CCC	181
Cys Ala Leu Gly	Gly Gly His Gly	Pro Gly Pro		
	20	25		

CCG	CAC	ACC	TGT	CCC	CAG	CGT	CGC	CTG	GGA	GCG	214
Pro	His	Thr	Cys	Pro	Gln	Arg	Arg	Leu	Gly	Ala	
			30						35		
CGC	GAC	CGG	GAC	ATG	CAG	CGT	GAA	ATC	CTG	CCG	247
Arg	Asp	Arg	Asp	Met	Gln	Arg	Glu	Ile	Leu	Pro	
			40						45		
GTG	CTC	GGG	CTA	CCG	GGA	CGC	CCC	GAC	CCC	GTG	280
Val	Leu	Gly	Leu	Pro	Gly	Arg	Pro	Asp	Pro	Val	
			50						55		
CAC	AAC	CCG	CCG	CTG	CCC	GGC	ACG	CAG	CGT	GCG	313
His	Asn	Pro	Pro	Leu	Pro	Gly	Thr	Gln	Arg	Ala	
						65				70	
CCC	CTC	TTC	ATG	TTG	GAC	CTA	TAC	CAC	GCC	ATG	346
Pro	Leu	Phe	Met	Leu	Asp	Leu	Tyr	His	Ala	Met	
						75				80	
ACC	GAT	GAC	GAC	GAC	GGC	GGG	CCA	CCA	CAG	GCT	379
Thr	Asp	Asp	Asp	Asp	Gly	Gly	Pro	Pro	Gln	Ala	
						85				90	
CAC	TTA	GGC	CGT	GCC	GAC	CTG	GTC	ATG	AGC	TTC	412
His	Leu	Gly	Arg	Ala	Asp	Leu	Val	Met	Ser	Phe	
						95				100	
GTC	AAC	ATG	GTG	GAA	CGC	GAC	CGT	ACC	CTG	GGC	445
Val	Asn	Met	Val	Glu	Arg	Asp	Arg	Thr	Leu	Gly	
						105				110	
TAC	CAG	GAG	CCA	CAC	TGG	AAG	GAA	TTC	CAC	TTT	478
Tyr	Gln	Glu	Pro	His	Trp	Lys	Glu	Phe	His	Phe	
						115				120	
										125	
GAC	CTA	ACC	CAG	ATC	CCT	GCT	GGG	GAG	GCT	GTC	511
Asp	Leu	Thr	Gln	Ile	Pro	Ala	Gly	Glu	Ala	Val	
						130				135	
ACA	GCT	GCT	GAG	TTC	CGG	ATC	TAC	AAA	GAA	CCC	544
Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Glu	Pro	
						140				145	

AGC	ACC	CAC	CCG	CTC	AAC	ACA	ACC	CTC	CAC	ATC	577
Ser	Thr	His	Pro	Leu	Asn	Thr	Thr	Leu	His	Ile	
		150						155			
AGC	ATG	TTC	GAA	GTG	GTC	CAA	GAG	CAC	TCC	AAC	610
Ser	Met	Phe	Glu	Val	Val	Gln	Glu	His	Ser	Asn	
		160						165			
AGG	GAG	TCT	GAC	TTG	TTC	TTT	TTG	GAT	CTT	CAG	643
Arg	Glu	Ser	Asp	Leu	Phe	Phe	Leu	Asp	Leu	Gln	
		170				175				180	
ACG	CTC	CGA	TCT	GGG	GAC	GAG	GGC	TGG	CTG	GTG	676
Thr	Leu	Arg	Ser	Gly	Asp	Glu	Gly	Trp	Leu	Val	
				185						190	
CTG	GAC	ATC	ACA	GCA	GCC	AGT	GAC	CGA	TGG	CTG	709
Leu	Asp	Ile	Thr	Ala	Ala	Ser	Asp	Arg	Trp	Leu	
			195					200			
CTG	AAC	CAT	CAC	AAG	GAC	CTG	GGA	CTC	CGC	CTC	742
Leu	Asn	His	His	Lys	Asp	Leu	Gly	Leu	Arg	Leu	
		205						210			
TAT	GTG	GAA	ACC	GCG	GAT	GGG	CAC	AGC	ATG	GAT	775
Tyr	Val	Glu	Thr	Ala	Asp	Gly	His	Ser	Met	Asp	
		215						220			
CCT	GGC	CTG	GCT	GGT	CTG	CTT	GGA	CGA	CAA	GCA	808
Pro	Gly	Leu	Ala	Gly	Leu	Leu	Gly	Arg	Gln	Ala	
		225				230				235	
CCA	CGC	TCC	AGA	CAG	CCT	TTC	ATG	GTA	ACC	TTC	841
Pro	Arg	Ser	Arg	Gln	Pro	Phe	Met	Val	Thr	Phe	
				240						245	
TTC	AGG	GCC	AGC	CAG	AGT	CCT	GTG	CGG	GCC	CCT	874
Phe	Arg	Ala	Ser	Gln	Ser	Pro	Val	Arg	Ala	Pro	
			250					255			
CGG	GCA	GCG	AGA	CCA	CTG	AAG	AGG	AGG	CAG	CCA	907
Arg	Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln	Pro	
		260						265			

AAG AAA ACG AAC GAG CTT CCG CAC CCC AAC AAA	940
Lys Lys Thr Asn Glu Leu Pro His Pro Asn Lys	
270 275	
CTC CCA GGG ATC TTT GAT GAT GGC CAC GGT TCC	973
Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser	
280 285 290	
CGC GGC AGA GAG GTT TGC CGC AGG CAT GAG CTC	1006
Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu	
295 300	
TAC GTC AGA TTC CGT GAC CTT GGC TGG CTG GAC	1039
Tyr Val Arg Phe Arg Asp Leu Gly Trp Leu Asp	
305 310	
TGG GTC ATC GCC CCC CAG GGC TAC TCT GCC TAT	1072
Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr	
315 320	
TAC TGT GAG GGG GAG TGT GCT TTC CCA CTG GAC	1105
Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp	
325 330	
TCC TGT ATG AAC GCC ACC AAC CAT GCC ATC TTG	1138
Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu	
335 340 345	
CAG TCT CTG GTG CAC CTG ATG AAG CCA GAT GTT	1171
Gln Ser Leu Val His Leu Met Lys Pro Asp Val	
350 355	
GTC CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG	1204
Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu	
360 365	
AGT GCC ACC TCT GTG CTG TAC TAT GAC AGC AGC	1237
Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser	
370 375	
AAC AAT GTC ATC CTG CGT AAA CAC CGT AAC ATG	1270
Asn Asn Val Ile Leu Arg Lys His Arg Asn Met	
380 385	

GTG GTC AAG GCC TGT GGC TGC CAC	1294
Val Val Lys Ala Cys Gly Cys His	
390 400	
TGAGGCCCCG CCCAGCATCC TGCTTCTACT ACCTTACCAT	1334
CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT	1374
TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT	1414
CCCCTGGCCA CTTCTGCTA AAATTCTGGT CTTTCCCAGT	1454
TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCACCCCGCC	1494
CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC	1534
AGCATCCCAG AGCTATGCTA ACTGAGAGGT CTGGGGTCAG	1574
CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC	1614
CTCAGCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGCC	1654
CTGGAATTCT AAAC TAGATG ATCTGGGCTC TCTGCACCAT	1694
TCATTGTGGC AGTTGGGACA TTTT TAGGTA TAACAGACAC	1734
ATACACTTAG ATCAATGCAT CGCTGTACTC CTTGAAATCA	1774
GAGCTAGCTT GTTAGAAAAA GAATCAGAGC CAGGTATAGC	1814
GGTGCATGTC ATTAATCCCA GCGCTAAAGA GACAGAGACA	1854
GGAGAATCTC TGTGAGTTCA AGGCCACATA GAAAGAGCCT	1894
GTCTCGGGAG CAGGAAAAAA AAAAAAACG GAATTC	1930

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
10					15			

Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Val	His	Gly	Ser	His	Gly	Arg	Gln
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	Ala	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His.					

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1956 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Bovinae
(F) TISSUE TYPE: bone
(vii) IMMEDIATE SOURCE:
(A) LIBRARY: human hippocampus
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGAATTCCGG	CCACAGTGGC	GCCGGCAGAG	CAGGAGTGGC	40
TGGAGGAGCT	GTGGTTGGAG	CAGGAGGTGG	CACGGCAGGG	80
CTGGAGGGCT	CCCTATGAGT	GGCGGAGACG	GCCCAGGAGG	120
CGCTGGAGCA	ACAGCTCCCA	CACCGCACCA	AGCGGTGGCT	160
GCAGGAGCTC	GCCCATCGCC	CCTGCGCTGC	TCGGACCGCG	200
GCCACAGCCG	GACTGGCGGG	TACGGCGGCG	ACAGAGGCAT	240
TGGCCGAGAG	TCCCAGTCCG	CAGAGTAGCC	CCGGCCTCGA	280
GGCGGTGGCG	TCCCGGTCCT	CTCCGTCCAG	GAGCCAGGAC	320
AGGTGTCGCG	CGGCGGGGCT	CCAGGGACCG	CGCCTGAGGC	360
CGGCTGCCCC	CCCGTCCCGC	CCCGCCCCGC	CGCCCGCCGC	400
CCGCCGAGCC	CAGCCTCCTT	GCCGTCGGGG	CGTCCCCAGG	440
CCCTGGGTCG	GCCGCGGAGC	CGATGCGCGC	CCGCTGAGCG	480
CCCCAGCTGA	GCGCCCCCGG	CCTGCC ATG	ACC GCG CTC	518
		Met Thr Ala Leu		
		1		

CCC	GGC	CCG	CTC	TGG	CTC	CTG	GGC	CTG	GCG	CTA	551
Pro	Gly	Pro	Leu	Trp	Leu	Leu	Gly	Leu	Ala	Leu	
5				10					15		
TGC	GCG	CTG	GGC	GGG	GGC	GGC	CCC	GGC	CTG	CGA	584
Cys	Ala	Leu	Gly	Gly	Gly	Gly	Pro	Gly	Leu	Arg	
			20						25		

CCC	CCG	CCC	GGC	TGT	CCC	CAG	CGA	CGT	CTG	GGC	617
Pro	Pro	Pro	Gly	Cys	Pro	Gly	arg	Arg	Leu	Gly	
			30					35			
GCG	CGC	GAC	CGG	GAC	GTG	CAG	CGC	GAG	ATC	CTG	650
Ala	Arg	Asp	Arg	Asp	Val	Gln	Arg	Glu	Ile	Leu	
		40					45				
GCG	GTG	CTC	GGG	CTG	CCT	GGG	CGG	CCC	CGG	CCC	683
Ala	Val	Leu	Gly	Leu	Pro	Gly	Arg	Pro	Arg	Pro	
	50					55					
CGC	GCG	CCA	CCC	GCC	GCC	TCC	CGG	CTG	CCC	GCG	716
Arg	Ala	Pro	Pro	Ala	Ala	Ser	Arg	Leu	Pro	Ala	
60					65					70	
TCC	GCG	CCG	CTC	TTC	ATG	CTG	GAC	CTG	TAC	CAC	749
Ser	Ala	Pro	Leu	Phe	Met	Leu	Asp	Leu	Tyr	His	
				75					80		
CGC	ATG	GCC	GGC	GAC	GAC	GAC	GAG	GAC	GGC	GCC	782
Arg	Met	Ala	Gly	Asp	Asp	Asp	Glu	Asp	Gly	Ala	
			85					90			
GCG	GAG	GCC	CTG	GGC	CGC	GCC	GAC	CTG	GTC	ATG	815
Ala	Glu	Ala	Leu	Gly	Arg	Ala	Asp	Leu	Val	Met	
		95					100				
AGC	TTC	GTT	AAC	ATG	GTG	GAG	CGA	GAC	CGT	GCC	848
Ser	Phe	Val	Asn	Met	Val	Glu	Arg	Asp	Arg	Ala	
	105					110					
CTG	GGC	CAC	CAG	GAG	CCC	CAT	TGG	AAG	GAG	TTC	881
Leu	Gly	His	Gln	Glu	Pro	His	Trp	Lys	Glu	Phe	
115					120					125	
CGC	TTT	GAC	CTG	ACC	CAG	ATC	CCG	GCT	GGG	GAG	914
Arg	Phe	Asp	Leu	Thr	Gln	Ile	Pro	Ala	Gly	Glu	
				130					135		
GCG	GTC	ACA	GCT	GCG	GAG	TTC	CGG	ATT	TAC	AAG	947
Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	
			140					145			

GTG	CCC	AGC	ATC	CAC	CTG	CTC	AAC	AGG	ACC	CTC	980
Val	Pro	Ser	Ile	His	Leu	Leu	Asn	Arg	Thr	Leu	
		150					155				
CAC	GTC	AGC	ATG	TTC	CAG	GTG	GTC	CAG	GAG	CAG	1013
His	Val	Ser	Met	Phe	Gln	Val	Val	Gln	Glu	Gln	
	160				165						
TCC	AAC	AGG	GAG	TCT	GAC	TTG	TTC	TTT	TTG	GAT	1046
Ser	Asn	Arg	Glu	Ser	Asp	Leu	Phe	Phe	Leu	Asp	
170					175					180	
CTT	CAG	ACG	CTC	CGA	GCT	GGA	GAC	GAG	GGC	TGG	1079
Leu	Gln	Thr	Leu	Arg	Ala	Gly	Asp	Glu	Gly	Trp	
				185						190	
CTG	GTG	CTG	GAT	GTC	ACA	GCA	GCC	AGT	GAC	TGC	1112
Leu	Val	Leu	Asp	Val	Thr	Ala	Ala	Ser	Asp	Cys	
			195					200			
TGG	TTG	CTG	AAG	CGT	CAC	AAG	GAC	CTG	GGA	CTC	1145
Trp	Leu	Leu	Lys	Arg	His	Lys	Asp	Leu	Gly	Leu	
		205					210				
CGC	CTC	TAT	GTG	GAG	ACT	GAG	GAC	GGG	CAC	AGC	1178
Arg	Leu	Tyr	Val	Glu	Thr	Glu	Asp	Gly	His	Ser	
	215					220					
GTG	GAT	CCT	GGC	CTG	GCC	GGC	CTG	CTG	GGT	CAA	1211
Val	Asp	Pro	Gly	Leu	Ala	Gly	Leu	Leu	Gly	Gln	
225					230					235	
CGG	GCC	CCA	CGC	TCC	CAA	CAG	CCT	TTC	GTG	GTC	1244
Arg	Ala	Pro	Arg	Ser	Gln	Gln	Pro	Phe	Val	Val	
				240						245	
ACT	TTC	TTC	AGG	GCC	AGT	CCG	AGT	CCC	ATC	CGC	1277
Thr	Phe	Phe	Arg	Ala	Ser	Pro	Ser	Pro	Ile	Arg	
			250					255			
ACC	CCT	CGG	GCA	GTG	AGG	CCA	CTG	AGG	AGG	AGG	1310
Thr	Pro	Arg	Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	
		260					265				

CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC	1343
Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala	
270 275	
AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC	1376
Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His	
280 285 290	
GGC TCC CAC GGC CGG CAG GTC TGC CGT CGG CAC	1409
Gly Ser His Gly Arg Gln Val Cys Arg Arg His	
295 300	
GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG	1442
Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp	
305 310	
CTG GAC TGG GTC ATC GCT CCC CAA GGC TAC TCG	1475
Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser	
315 320	
GCC TAT TAC TGT GAG GGG GAG TGC TCC TTC CCA	1508
Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro	
325 330	
CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC	1541
Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala	
335 340 345	
ATC CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA	1574
Ile Leu Gln Ser Leu Val His Leu Met Lys Pro	
350 355	
AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC	1607
Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr	
360 365	
AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC	1640
Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp	
370 375	
AGC AGC AAC AAC GTC ATC CTG CGC AAA GCC CGC	1673
Ser Ser Asn Asn Val Ile Leu Arg Lys Ala Arg	
380 385	

AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC	1703
Asn Met Val Val Lys Ala Cys Gly Cys His	
390	395
TGAGTCAGCC CGCCCAGCCC TACTGCAGCA ATTCAGTGGC	1743
CGTCGTTTTTA CAACGTGTGA CTGGGAAAAC CCTGGCGTTA	1783
CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG	1823
CTGGCTAATA GCGAAGAGGC CCCGCACCGA TCGCCCTTCC	1863
CAACAGTTGC GCCCCAGTGA ATGGCGAATG GCAAATTGTA	1903
AGCGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTTT	1941

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys Xaa ₁ Xaa ₂ His Glu Leu Tyr Val Xaa ₃ Phe	
1	10
Xaa ₄ Asp Leu Gly Trp Xaa ₅ Asp Trp Xaa ₆ Ile	
15	20
Ala Pro Xaa ₇ Gly Tyr Xaa ₈ Ala Tyr Tyr Cys	
25	30
Glu Gly Cys Xaa ₉ Phe Pro Leu Xaa ₁₀ Ser Xaa ₁₁	
35	40
Met Asn Ala Thr Asn His Ala Ile Xaa ₁₂ Thr	
45	50
Leu Xaa ₁₃ Xaa ₁₄ Xaa ₁₅ Xaa ₁₆ Xaa ₁₇ Xaa ₁₈ Val	
55	
Pro Lys Xaa ₁₉ Cys Cys Ala Pro Thr Xaa ₂₀ Leu	
60	65

Xaa₂₁ Ala Xaa₂₂ Ser Val Leu Tyr Xaa₂₃ Asp
70 75

Xaa₂₄ Ser Xaa₂₅ Asn Val Xaa₂₆ Leu Xaa₂₇ Lys
80 85

Xaa₂₈ Pro Asn Met Val Val Xaa₂₉ Ala Cys Gly
90 95

Cys His,

wherein Xaa₁ = (Lys or Arg); Xaa₂ = (Lys or Arg);
Xaa₃ = (Ser or Arg); Xaa₄ = (Arg or Gln); Xaa₅ =
(Gln or Leu); Xaa₆ = (Ile or Val); Xaa₇ = (Glu or
Gln); Xaa₈ = (Ala or Ser); Xaa₉ = (Ala or Ser);
Xaa₁₀ = (Asn or Asp); Xaa₁₁ = (Tyr or Cys); Xaa₁₂ =
(Val or Leu); Xaa₁₃ = (His or Asn); Xaa₁₄ = (Phe or
Leu); Xaa₁₅ = (Ile or Met); Xaa₁₆ = (Asn or Lys);
Xaa₁₇ = (Glu, Asp or Asn); Xaa₁₈ = (Thr, Ala or
Val); Xaa₁₉ = (Pro or Ala); Xaa₂₀ = (Gln or Lys);
Xaa₂₁ = (Asn or Ser); Xaa₂₂ = (Ile or Thr); Xaa₂₃ =
(Phe or Tyr); Xaa₂₄ = (Asp, Glu or Ser); Xaa₂₅ =
(Ser or Asn); Xaa₂₆ = (Ile or Asp); Xaa₂₇ = (Lys or
Arg); Xaa₂₈ = (Tyr, Ala or His); and Xaa₂₉ = (Arg
or Lys).

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Bovinae
 (F) TISSUE TYPE: bone
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: human placenta
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

	TCC ACG GGG	9
	Ser Thr Gly	
	1	
AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG	42	
Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr		
5 10		
CCC AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC	75	
Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn		
15 20 25		
GTG GCA GAG AAC AGC AGC AGC GAC CAG AGG CAG	108	
Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln		
30 35		
GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC	141	
Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe		
40 45		
CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG	174	
Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala		
50 55		
CCT GAA GGC TAC GCC GCC TAC TAC TGT GAG GGG	207	
Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly		
60 65		
GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC	240	
Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn		
70 75 80		
GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC	273	
Ala Thr Asn His Ala Ile Val Gln Thr Leu Val		
85 90		

CAC TTC ATC AAC CCG GAA ACG GTG CCC AAG CCC	306
His Phe Ile Asn Pro Glu Thr Val Pro Lys Pro	
95 100	
TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC	339
Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser	
105 110	
GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC	372
Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile	
115 120	
CTG AAG AAA TAC AGA AAC ATG GTG GTC CGG GCC	405
Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala	
125 130 135	
TGT GGC TGC CAC TAGCTCCTCC GAGAATTCAG	437
Cys Gly Cys His	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
1 5 10	
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
15 20	
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa	
25 30	
Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa	
35 40	
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
45 50 55	

```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
      60                      65
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      70                      75
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      80                      85
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
      90                      95
Xaa Cys Xaa,
100

```

wherein each Xaa independently represents one of the 20 naturally occurring L-isomer, α -amino acids.

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1                      5                      10
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      15                      20
Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
      25                      30
Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      35                      40
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
45                      50                      55

```

```

Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa
      60                      65
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      70                      75
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      80                      85
Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa,
      90                      95

```

wherein each Xaa independently represents one of the 20 naturally occurring L-isomer, α -amino acids.

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

          Pro  Leu  Arg  Arg  Arg  Gln
           1                      5
Pro  Lys  Lys  Ser  Asn  Glu  Leu  Pro  Gln
          10                      15
Ala  Asn  Arg  Leu  Pro  Gly  Ile  Phe  Asp
          20
Asp  Val  Asn  Gly  Ser  His  Gly  Arg  Gln
 25                      30
Val  Cys  Arg  Arg  His  Glu  Leu  Tyr  Val
 35                      40
Ser  Phe  Gln  Asp  Leu  Gly  Trp  Leu  Asp
          45                      50

```

Tyr	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
			55					60
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
				65				
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
70					75			
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
	80					85		
Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
		90					95	
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
			100					105
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
				110				
Asp	Glu	Ser	Asn	Asn	Val	Ile	Leu	Arg
115					120			
Lys	Ala	Arg	Asn	Met	Val	Val	Lys	Ala
	125					130		
Cys	Gly	Cys	His.					
		135						

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

						Arg	Arg	Gln
						1		
Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
	5					10		

Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
		15					20	
Asp	Val	Asn	Gly	Ser	His	Gly	Arg	Gln
			25					30
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
				35				
Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
40					45			
Tyr	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
	50					55		
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
		60					65	
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
			70					75
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
				80				
Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
85					90			
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
	95					100		
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
		105					110	
Asp	Glu	Ser	Asn	Asn	Val	Ile	Leu	Arg
			115					120
Lys	Ala	Arg	Asn	Met	Val	Val	Lys	Ala
				125				
Cys	Gly	Cys	His.					
130								

(2)

INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

						Ser 1	Gln	Gln
Pro	Phe 5	Val	Val	Thr	Phe	Phe 10	Arg	Ala
Ser	Pro	Ser 15	Pro	Ile	Arg	Thr	Pro 20	Arg
Ala	Val	Arg	Pro 25	Leu	Arg	Arg	Arg	Gln 30
Pro	Lys	Lys	Ser	Asn 35	Glu	Leu	Pro	Gln
Ala 40	Asn	Arg	Leu	Pro	Gly 45	Ile	Phe	Asp
Asp 50	Val	Asn	Gly	Ser	His	Gly 55	Arg	Gln
Val	Cys	Arg 60	Arg	His	Glu	Leu	Tyr 65	Val
Ser	Phe	Gln	Asp 70	Leu	Gly	Trp	Leu	Asp 75
Tyr	Val	Ile	Ala	Pro 80	Gln	Gly	Tyr	Ser
Ala 85	Tyr	Tyr	Cys	Glu	Gly 90	Glu	Cys	Ser
Phe	Pro 95	Leu	Asp	Ser	Cys	Met 100	Asn	Ala
Thr	Asn	His 105	Ala	Ile	Leu	Gln	Ser 110	Leu
Val	His	Leu	Met 115	Lys	Pro	Asn	Ala	Val 120
Pro	Lys	Ala	Cys	Cys 125	Ala	Pro	Thr	Lys

Leu 130	Ser	Ala	Thr	Ser	Val 135	Leu	Tyr	Tyr
Asp	Glu 140	Ser	Asn	Asn	Val	Ile 145	Leu	Arg
Lys	Ala	Arg 150	Asn	Met	Val	Val	Lys 165	Ala
Cys	Gly	Cys	His. 170					